



US-162
SEQUENCE LISTING

<110> Yumi Matsuzaki, Jun Nakamura and Kenichi Hashiguchi
<120> Method for producing L-arginine or L-lysine by fermentation
<130> US-162
<140> US/10/790,224
<141> 2004-03-02
<150> JP 2003-056129
<151> 2003-03-03
<160> 24
<170> PatentIn Ver. 2.0

<210> 1
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer for PCR

<400> 1
cccggtttt cttctgcaac tcggg 25

<210> 2
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer for PCR

<400> 2
gtcgacaagc tcggttgttc ccagc 25

<210> 3
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer for PCR

<400> 3
cccctagttc aaggcttgtt aatc 24

<210> 4
<211> 25
<212> DNA

US-162

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for PCR

<400> 4

gtcttacctc ggctgggtgg ccagc

25

<210> 5

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 5

agaactacga gtccgccttt ttg

23

<210> 6

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 6

cgtatcacca g caacccacgc a

21

<210> 7

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 7

cttcccagta gcaccatacg ac

22

<210> 8

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 8

ctgggtggcag ttcgaagagg tccttg

26

<210> 9

<211> 26

<212> DNA

US-162

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 9

ggacaaggac ctcttcgaac tgccag

26

<210> 10

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 10

cggcgagacc gtcgattggg aggagc

26

<210> 11

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 11

gtagcacctt acgaccaaac cg

22

<210> 12

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 12

ggagccggtc gacgaggagc

20

<210> 13

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 13

gccccgggca ggcaagaatc ctc

23

<210> 14

<211> 21

<212> DNA

US-162

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 14

tccccgggag gctctctgca g

21

<210> 15

<211> 4235

<212> DNA

<213> Brevibacterium flavum

<220>

<221> CDS

<222> (1852)..(2364)

<400> 15

aaaccgggt tttcttctgc aactcggcg ccgaaggaaa cgaggctgct ttcaagattg 60
cacgcttgcac tggtcgttcc cggattctgg ctgcagttca tggtttccac ggccgcacca 120
tgggtccct cgcgtgact ggccagccag acaagcgtga agcgttctg ccaatgccaa 180
gcgggttggaa gttctaccc tacggcgaca cggattactt gcgcggaaatg gtagaaacca 240
acccaacgga tggcgttgc atcttcctcg agccaatcca gggtaaacg ggcgttggc 300
cagcacctga aggattccctc aaggcagtgc gcgagctgtg cgatgagttac ggcacatcttga 360
tgatcaccga tgaagtccag actggcggtt gccgttcccg cgatttctt gcacatcagc 420
acgatggcgat tgggttcccgat gtgggttacca tggccaaagggg acttggcgcc ggtttccca 480
tcgggttgc tttggccact ggccgtgcag ctgaatttgc gaccccaggc aagcacggca 540
ccacttccgg tggcaacccca gttgttgc gagctgcacca ggcagtgtgc tctgttgtcg 600
atgacgtttt ctgcgcagaaa gttacccgc agggcgagct gttcaaggta cttcttgcca 660
aggttgcggg ctttgcgttgc acggcgatcc ggggttgc gttggcggtg gtgctggagc 720
gchgacgtcgaa aagcaagact gtttttgc gtttttgc gggcggttatt ttgaatgcac 780
cgccggacaa cattatccgt ttgacccgcg cgctgttgc caccgacgaa gaaatgcag 840
acgcagtcaa ggcttattgcc gagacaatcg cataaaaggac ttaaacttat gacttcacaa 900
ccacagggttcc gccatttccct ggctgttgc gatctcaccct ctgcagagca ggcagaggtt 960
ttgaccccttgc cgcggaaatgc caaggcgacg ccgttttgcg agcgttccact cgagggacca 1020
aagtccgttgc cagtttttgc tgataaagact tcaactcgttca ctcgtttctc cttcgacgcg 1080
ggcatcgatc attttgggtgg acatggccatc gtcgttgc gtcgttgc acagatgggt 1140
aaggggcgaga ccctgcggaa caccggcgat gtatttttgc gtcgttgc agcaatttgc 1200
tggcgccacctt acgcacacac caattttccac gccatggcg agacgttccact tggccgttgc 1260
gtgaacttccct tggccgtatc tctgcacccca tgccgttgc tggttgc gtcgttgc tgcagaccatc 1320
gtggaaaaacc tcagccctgaa agaaggccca gcaggccatc aggttgc ggcgttgtac 1380
ctggcgatc gcgacaacaa catggccac tcctacatgc ttggccatc caccgcgggc 1440
atggatattt ccatcatcgcc tcctgttgcggttccatc ttccagccctc tgccgttgc cgtggagcgc 1500
gcggaaaaacc gcgttgcgatc aaccggcgacg aagggttgc tcaccgcacag cctcgacgag 1560
gttgcggcgcc cccatgttgc tttccatc acctgggtat ccatgggtat ggaaaacgcac 1620
ggcatcgatc gcaccacacc ttccatc taccaggatc acgttgcgatc catggcgaaa 1680
gctaaccgcg gcgccatctt cctgcactgc ttccatc accggcgacg agaagtggca 1740
gcctccgttgc ttgttgcgatc agcgttgcgatc gtttttgc gtcgttgc tgcagaccatc 1800
gctcagaaatgc cactgttgcgttgc gccaaccgcg cgaggtaaga c atg tct 1857
Met Ser
1

ctt ggc tca acc ccg tca aca ccg gaa aac tta aat ccc gtg act cgc 1905
Leu Gly Ser Thr Pro Ser Thr Pro Glu Asn Leu Asn Pro Val Thr Arg

5

10

15

act gca cgc caa gct ctc att ttg cag att ttg gac aaa caa aaa gtc 1953

US-162

Thr Ala Arg Gln Ala Leu Ile Leu Gln Ile Leu Asp Lys Gln Lys Val	
20 25 30	
acc agc cag gta caa ctg tct gaa ttg ctg ctg gat gaa ggc atc gat	2001
Thr Ser Gln Val Gln Leu Ser Glu Leu Leu Asp Glu Gly Ile Asp	
35 40 45 50	
atc acc cag gcc acc ttg tcc cg gat ctc gat gaa ctc ggt gca cgc	2049
Ile Thr Gln Ala Thr Leu Ser Arg Asp Leu Asp Glu Leu Gly Ala Arg	
55 60 65	
aag gtt cgc ccc gat ggg gga cgc gcc tac tac gcg gtc ggc cca gta	2097
Lys Val Arg Pro Asp Gly Gly Arg Ala Tyr Tyr Ala Val Gly Pro Val	
70 75 80	
gat agc atc gcc cgc gaa gat ctc cgg ggt ccg tcg gag aag ctg cgc	2145
Asp Ser Ile Ala Arg Glu Asp Leu Arg Gly Pro Ser Glu Lys Leu Arg	
85 90 95	
cgc atg ctt gat gaa ctg ctg gtt tct aca gat cat tcc ggc aac atc	2193
Arg Met Leu Asp Glu Leu Leu Val Ser Thr Asp His Ser Gly Asn Ile	
100 105 110	
gct atg ctg cgc acc ccg ccg gga gct gcc cag tac ctg gca agt ttc	2241
Ala Met Leu Arg Thr Pro Pro Gly Ala Ala Gln Tyr Leu Ala Ser Phe	
115 120 125 130	
atc gat agg gtg ggg ctg aaa gaa gtc gtt ggc acc atc gct ggc gat	2289
Ile Asp Arg Val Gly Leu Lys Glu Val Val Gly Thr Ile Ala Gly Asp	
135 140 145	
gac acc gtt ttt gtt ctc gcc cgt gat ccg ctc aca ggt aaa gaa cta	2337
Asp Thr Val Phe Val Leu Ala Arg Asp Pro Leu Thr Gly Lys Glu Leu	
150 155 160	
ggt gaa tta ctc agc ggg cgc acc act taaagcgccc cttagttcaag	2384
Gly Glu Leu Leu Ser Gly Arg Thr Thr	
165 170	
gcttgttaat cgcttgttaa tgcaggcagg taaggtataa cccgagtgtt ttttcgagga	2444
ataccaaccc tttcaacaca ataattttct ttaaacatcc ttgtgttcca ccacggctgg	2504
caaggaacctt aaaatgaagg agcacaccc tc atgactaacc gc atcgttct tgcatactcc	2564
ggcggtctgg acaccactgt ggcaattcca tacctgaaga agatgattga tggtaagtc	2624
atcgcattt ctctcgaccc gggccagggt ggagagaaca tggacaacgt tcgcccagcgt	2684
gcattggatg cgggtgcagc tgagtccatc gttgttgatg caaaggatga ttgcgttag	2744
gagtactgcc tgccaaaccat caaggcaa ac ggc atgtaca tgaagcagta cccactgggt	2804
tctgcaatct cccgcccact gatcgtcaag cacctcggtt aggctggcaa gcagttcaac	2864
ggtaccacag ttgcacacgg ctgcacttgtt aaggccaacg accagggttcg ttgcagggtc	2924
ggcttcatgg acaccgatcc aaacctggag atcattgcac ctgcgtgtt cttcgcatgg	2984
accccgacca aggctatcgc cttcgccgag gagaacaacg ttccaatcga gcagtccgtg	3044
aagtccccat tctccatcga ccagaacgtc tggggccgcg ctattgagac cggttacctg	3104
gaagatctgt ggaatgctcc aaccaaggac atctacgc acaccgagga tccagctctg	3164
ggtaacgctc cagatgaggt catcatctcc ttgcagggtt gcaagccagt ctccatcgat	3224
ggccgtccag tctccgtact gcaggctatt gaagagctga accgtcgtgc aggccgcacag	3284
ggcgttggcc gccttgcacat gtttggggac cgtctcggtt gcatcaagtc cccgaaatc	3344
tacgaagcac caggcgcaat cgcactgatt aaggctc acaggcttttggaa agatgtcacc	3404
atcgagcgcg aactggctcg ctacaagcgt ggcgttgcac cacgttggc tgaggaagta	3464
tacgacggcc tgggttccgg acctctgaag cgctccctgg acgcgttcat tgattccacc	3524
caggagcacg tcaccggcga tatccgcac gttctgcacg cagggttccat caccatcaat	3584
ggtcgtcggtt ccagccactc cctgtacgac ttcaacctgg ctacatcga caccggcgac	3644
accttcgacc agaccctggc taagggtttt gtccagctgc acggctgtc ctccaaagatc	3704
gctaacaaggc gcgatcgca agctggcaac aactaaggca ccttttcaag catccagact	3764
agaacttcaa gtatggaa agtagaaaggaa caccatcg aacagcacgg aaccaatgaa	3824
ggtgcgctgt gggcgcccg ctctccggt ggaccctccg aggccatgtt cgccttgagt	3884
gtctccactc atttcgactg ggttttggcc ccttatgatg tggggcctc caaggcacac	3944

US-162

gccaaggttt tgcaccaagc agagctactt tctgatgaag atcttagccac catgctggct 4004
 ggtcttgcgc agctgggcaa ggatgtcgcc gacggAACCT tcggTCCGCT gccttctgat 4064
 gaggatgtgc acggcgcgat ggaacgcggt ctgattgacc gcgttggtcc tgaggtggc 4124
 ggccgtctgc ggcgtggtcg ttcccgaac gaccagggtgg caaccctgtt ccgcatgtgg 4184
 gtccgcgacg cagtgcgcga catgcgcgtg ggaacaaccg agcttgtcga C 4235

<210> 16

<211> 171

<212> PRT

<213> *Brevibacterium flavum*

<400> 16

Met	Ser	Leu	Gly	Ser	Thr	Pro	Ser	Thr	Pro	Glu	Asn	Leu	Asn	Pro	Val
1															15
Thr	Arg	Thr	Ala	Arg	Gln	Ala	Leu	Ile	Leu	Gln	Ile	Leu	Asp	Lys	Gln
															20
Lys	Val	Thr	Ser	Gln	Val	Gln	Leu	Ser	Glu	Leu	Leu	Leu	Asp	Glu	Gly
															25
Ile	Asp	Ile	Thr	Gln	Ala	Thr	Leu	Ser	Arg	Asp	Leu	Asp	Glu	Leu	Gly
															30
Ala	Arg	Lys	Val	Arg	Pro	Asp	Gly	Gly	Arg	Ala	Tyr	Tyr	Ala	Val	Gly
															35
Pro	Val	Asp	Ser	Ile	Ala	Arg	Glu	Asp	Leu	Arg	Gly	Pro	Ser	Glu	Lys
															40
Leu	Arg	Arg	Met	Leu	Asp	Glu	Leu	Leu	Val	Ser	Thr	Asp	His	Ser	Gly
															45
Asn	Ile	Ala	Met	Leu	Arg	Thr	Pro	Pro	Gly	Ala	Ala	Gln	Tyr	Leu	Ala
															50
Ser	Phe	Ile	Asp	Arg	Val	Gly	Leu	Lys	Glu	Val	Val	Gly	Thr	Ile	Ala
															55
Gly	Asp	Asp	Thr	Val	Phe	Val	Leu	Ala	Arg	Asp	Pro	Leu	Thr	Gly	Lys
															60
Glu	Leu	Gly	Glu	Leu	Leu	Ser	Gly	Arg	Thr	Thr					
															65
															70
															75
															80
															85
															90
															95
															100
															105
															110
															115
															120
															125
															130
															135
															140
															145
															150
															155
															160
															165
															170

<210> 17

<211> 3138

<212> DNA

<213> *Brevibacterium lactofermentum*

<220>

<221> CDS

<222> (1)..(3138)

<400> 17

atg	tca	gga	ccg	tta	aga	agt	gaa	cgt	aaa	gtc	gtt	ggc	ttt	gtc	aga
Met	Ser	Gly	Pro	Leu	Arg	Ser	Glu	Arg	Lys	Val	Val	Gly	Phe	Val	Arg
1															48
gac	cca	ctg	cca	aaa	gtt	ggt	tct	tta	tcg	ctg	aaa	tct	gag	cat	gcc
Asp	Pro	Leu	Pro	Lys	Val	Gly	Ser	Leu	Ser	Leu	Lys	Ser	Glu	His	Ala
															20
															25
															30
caa	gca	gat	cta	gag	cat	ttg	ggt	tgg	cgc	aat	gtt	gag	tct	ttg	gat
Gln	Ala	Asp	Leu	Glu	His	Leu	Gly	Trp	Arg	Asn	Val	Glu	Ser	Leu	Asp
															35
															40
															45
ttg	ttg	tgg	ggc	ttg	tca	ggt	gca	ggc	gat	ccc	gat	gtc	gcg	ctg	aac

192

US-162

Leu	Leu	Trp	Gly	Leu	Ser	Gly	Ala	Gly	Asp	Pro	Asp	Val	Ala	Leu	Asn		
50			55			60											
ctt	ctt	att	cgg	ctg	tat	cag	gca	ctt	gaa	gca	atc	ggc	gag	gat	gct	240	
Leu	Leu	Ile	Arg	Leu	Tyr	Gln	Ala	Leu	Glu	Ala	Ile	Gly	Glu	Asp	Ala		
65			70			75										80	
cga	aac	gag	ctt	gat	caa	gag	att	cgc	cag	gat	gaa	gaa	cta	cga	gtc	288	
Arg	Asn	Glu	Leu	Asp	Gln	Glu	Ile	Arg	Gln	Asp	Glu	Glu	Leu	Arg	Val		
			85			90										95	
cgc	ctt	ttt	gca	ttg	ttg	ggt	ggt	tcc	tcg	gct	gtc	ggt	gat	cac	ttg	336	
Arg	Leu	Phe	Ala	Leu	Leu	Gly	Gly	Ser	Ser	Ala	Val	Gly	Asp	His	Leu		
			100			105										110	
gtc	gcc	aat	cct	ttg	cag	tgg	aaa	ctc	tta	aaa	ctt	gat	gcg	cca	tcg	384	
Val	Ala	Asn	Pro	Leu	Gln	Trp	Lys	Leu	Leu	Lys	Leu	Asp	Ala	Pro	Ser		
			115			120										125	
agg	gaa	gag	atg	ttt	cag	gcg	ctg	ctg	gaa	tct	gtg	aaa	gct	cag	cct	432	
Arg	Glu	Glu	Met	Phe	Gln	Ala	Leu	Leu	Glu	Ser	Val	Lys	Ala	Gln	Pro		
			130			135										140	
gct	gtg	ctt	gag	gtt	gag	gat	ttc	agc	gat	gca	cac	aac	att	gcc	cga	480	
Ala	Val	Leu	Glu	Val	Glu	Asp	Phe	Ser	Asp	Ala	His	Asn	Ile	Ala	Arg		
			145			150										160	
gac	gat	ttg	agc	acg	cct	ggt	ttt	tac	acg	gct	agt	gtt	acc	ggg	cct	528	
Asp	Asp	Leu	Ser	Thr	Pro	Gly	Phe	Tyr	Thr	Ala	Ser	Val	Thr	Gly	Pro		
			165			170										175	
gaa	gca	gag	cga	gtc	ttg	aaa	tgg	act	tat	cgc	acg	ttg	ctg	acc	cgg	576	
Glu	Ala	Glu	Arg	Val	Leu	Lys	Trp	Thr	Tyr	Arg	Thr	Leu	Leu	Thr	Arg		
			180			185										190	
att	gct	gcg	cat	gat	tta	gcg	ggt	acc	tat	ccc	acc	gac	atg	cgg	aga	624	
Ile	Ala	Ala	His	Asp	Leu	Ala	Gly	Thr	Tyr	Pro	Thr	Asp	Met	Arg	Arg		
			195			200										205	
aaa	ggt	ggc	gat	cct	gtt	ccg	ttt	agc	aca	gtg	acc	atg	cag	ctc	agc	672	
Lys	Gly	Gly	Asp	Pro	Val	Pro	Phe	Ser	Thr	Val	Thr	Met	Gln	Leu	Ser		
			210			215										220	
gac	cta	gct	gat	gct	gtt	act	gct	gct	tta	gct	gtg	gca	att	gcc		720	
Asp	Leu	Ala	Asp	Ala	Ala	Leu	Thr	Ala	Ala	Leu	Ala	Val	Ala	Ile	Ala		
			225			230										240	
aat	gtt	tat	ggt	gaa	aag	ccg	gtt	gat	tca	gct	tta	tct	gtc	atc	gcg	768	
Asn	Val	Tyr	Gly	Glu	Lys	Pro	Val	Asp	Ser	Ala	Leu	Ser	Val	Ile	Ala		
			245			250										255	
atg	ggc	aaa	tgt	ggc	gcg	cag	gaa	ttg	aac	tac	att	tca	gat	gtg	gac	816	
Met	Gly	Lys	Cys	Gly	Ala	Gln	Glu	Leu	Asn	Tyr	Ile	Ser	Asp	Val	Asp		
			260			265										270	
gtg	gtg	ttt	gtt	gca	gag	ccg	gca	aac	tct	aaa	tca	aca	cgc	acc	gca	864	
Val	Val	Phe	Val	Ala	Glu	Pro	Ala	Asn	Ser	Lys	Ser	Thr	Arg	Thr	Ala		
			275			280										285	
gca	gag	ctc	att	cgc	atc	ggt	agc	aac	tcg	ttc	ttt	gag	gtg	gat	gca	912	
Ala	Glu	Leu	Ile	Arg	Ile	Gly	Ser	Asn	Ser	Phe	Phe	Glu	Val	Asp	Ala		
			290			295										300	
gca	ctt	cgc	cca	gaa	ggt	aaa	agt	ggc	gct	ctt	gtg	cgc	tct	ttg	gat	960	
Ala	Leu	Arg	Pro	Glu	Gly	Lys	Ser	Gly	Ala	Leu	Val	Arg	Ser	Leu	Asp		
			305			310										320	
tcc	cat	atg	gcf	tat	tac	aag	cgc	tgg	gcf	gaa	acc	tgg	gaa	ttt	cag	1008	
Ser	His	Met	Ala	Tyr	Tyr	Lys	Arg	Trp	Ala	Glu	Thr	Trp	Glu	Phe	Gly		
			325			330										335	
gca	ctg	ctg	aaa	gct	cgt	ccc	atg	acg	ggt	gat	att	gac	ctt	ggg	cag	1056	
Ala	Leu	Leu	Lys	Ala	Arg	Pro	Met	Thr	Gly	Asp	Ile	Asp	Leu	Gly	Gln		

US-162

340	345	350	
tcc tat gtg gat gct ctt tca ccg ttg att tgg gcg gct agc cag cgg			1104
Ser Tyr Val Asp Ala Leu Ser Pro Leu Ile Trp Ala Ala Ser Gln Arg			
355 360 365			
gaa tca ttt gtc aca gat gtc caa gct atg cgc cgt cga gtg ttg gac			1152
Glu Ser Phe Val Thr Asp Val Gln Ala Met Arg Arg Arg Val Leu Asp			
370 375 380			
aat gtt ccg gaa gac ttg cgt gat cgt gag ctg aag ctt ggt cgc ggt			1200
Asn Val Pro Glu Asp Leu Arg Asp Arg Glu Leu Lys Leu Gly Arg Gly			
385 390 395 400			
ggt ttg agg gat gtg gag ttt gct gtc cag ctc ctt cag atg gtg cat			1248
Gly Leu Arg Asp Val Glu Phe Ala Val Gln Leu Leu Gln Met Val His			
405 410 415			
ggt cgc att gat gag acg ttg cgg gtt cgg tca acg gta aat gct ttg			1296
Gly Arg Ile Asp Glu Thr Leu Arg Val Arg Ser Thr Val Asn Ala Leu			
420 425 430			
cat gtg ttg gtt gat cag gga tat gtg ggt cgt gaa gac ggg cat aat			1344
His Val Leu Val Asp Gln Gly Tyr Val Gly Arg Glu Asp Gly His Asn			
435 440 445			
ctc att gag tcg tat gag ttt ttg cgc ctg ttg gag cat cgc ctt caa			1392
Leu Ile Glu Ser Tyr Glu Phe Leu Arg Leu Leu Glu His Arg Leu Gln			
450 455 460			
ttg gag cgg atc aag cgc act cac ttg tta ccg aaa cct gat gac cga			1440
Leu Glu Arg Ile Lys Arg Thr His Leu Leu Pro Lys Pro Asp Asp Arg			
465 470 475 480			
atg aat atg cgc tgg ttg gcg cgc gct tct ggg ttt act ggt tcg atg			1488
Met Asn Met Arg Trp Leu Ala Arg Ala Ser Gly Phe Thr Gly Ser Met			
485 490 495			
gag caa agt tcg gcc aaa gct atg gaa cgg cat ttg cgt aag gtt cgt			1536
Glu Gln Ser Ser Ala Lys Ala Met Glu Arg His Leu Arg Lys Val Arg			
500 505 510			
ttg cag att cag tcg ttg cat agt cag ctg ttt tat cgg cca ctg ctg			1584
Leu Gln Ile Gln Ser Leu His Ser Gln Leu Phe Tyr Arg Pro Leu Leu			
515 520 525			
aac tct gtg gtc aac ttg agc gcg gat gcc atc aga ttg tct ccg gat			1632
Asn Ser Val Val Asn Leu Ser Ala Asp Ala Ile Arg Leu Ser Pro Asp			
530 535 540			
gct gca aag cta caa ttg ggg gca ttg gga tac ctg cat cca tca cgt			1680
Ala Ala Lys Leu Gln Leu Gly Ala Leu Gly Tyr Leu His Pro Ser Arg			
545 550 555 560			
gct tat gaa cac ctg act gct ctt gca tca gga gct agc cgt aaa gcc			1728
Ala Tyr Glu His Leu Thr Ala Leu Ala Ser Gly Ala Ser Arg Lys Ala			
565 570 575			
aag att cag gcg atg ttg ctg ccc acg ttg atg gag tgg ctg tct caa			1776
Lys Ile Gln Ala Met Leu Leu Pro Thr Leu Met Glu Trp Leu Ser Gln			
580 585 590			
aca gct gaa cca gat gcg gga ttg ctg aat tac cgc aag ctt tct gat			1824
Thr Ala Glu Pro Asp Ala Gly Leu Leu Asn Tyr Arg Lys Leu Ser Asp			
595 600 605			
gct tcc tat gat cgc agc tgg ttt ttg cgc atg ctg cgt gat gag ggc			1872
Ala Ser Tyr Asp Arg Ser Trp Phe Leu Arg Met Leu Arg Asp Glu Gly			
610 615 620			
gta gtg ggg cag cgg ttg atg cgt att ttg gga aat tct ccc tat att			1920
Val Val Gly Gln Arg Leu Met Arg Ile Leu Gly Asn Ser Pro Tyr Ile			
625 630 635 640			

US-162

tct	gaa	ctg	att	atc	tcc	act	ccg	gac	ttt	gtg	aaa	cag	ctg	ggt	gat		1968
Ser	Glu	Leu	Ile	Ile	Ser	Thr	Pro	Asp	Phe	Val	Lys	Gln	Leu	Gly	Asp		
																655	
																645	650
gcg	gcg	tct	ggt	cct	aaa	ttg	ctt	gct	act	gca	ccg	act	cag	gtt	gtg		2016
Ala	Ala	Ser	Gly	Pro	Lys	Leu	Leu	Ala	Thr	Ala	Pro	Thr	Gln	Val	Val		
																660	665
																670	670
aaa	gca	atc	aag	gcg	acg	gtg	tcg	cgt	cat	gag	tca	cct	gat	cgg	gcg		2064
Lys	Ala	Ile	Lys	Ala	Thr	Val	Ser	Arg	His	Glu	Ser	Pro	Asp	Arg	Ala		
																675	680
																685	685
atc	cag	gct	gca	cga	tcg	ctg	agg	agg	cag	gag	ctg	gca	cgc	att	gcc		2112
Ile	Gln	Ala	Ala	Arg	Ser	Leu	Arg	Arg	Gln	Glu	Leu	Ala	Arg	Ile	Ala		
																690	695
																700	700
tct	gct	gat	ttg	ctc	aac	atg	ctc	act	gtt	cag	gaa	gta	tgc	caa	agc		2160
Ser	Ala	Asp	Leu	Leu	Asn	Met	Leu	Thr	Val	Gln	Glu	Val	Cys	Gln	Ser		
																705	710
																715	720
ttg	tca	cta	gtc	tgg	gat	gcg	gtg	ttg	gat	gct	gcc	ttg	gat	gcg	gaa		2208
Leu	Ser	Leu	Val	Trp	Asp	Ala	Val	Leu	Asp	Ala	Ala	Leu	Asp	Ala	Glu		
																725	730
																735	735
atc	cgt	gct	gca	ctt	aac	gat	cca	cag	aaa	cca	gat	cag	cct	ctg	gcc		2256
Ile	Arg	Ala	Ala	Leu	Asn	Asp	Pro	Gln	Lys	Pro	Asp	Gln	Pro	Leu	Ala		
																740	745
																750	750
aat	att	tct	gtg	atc	ggc	atg	ggc	cgt	ttg	ggt	gga	gca	gaa	ctt	gga		2304
Asn	Ile	Ser	Val	Ile	Gly	Met	Gly	Arg	Leu	Gly	Gly	Ala	Glu	Leu	Gly		
																755	760
																765	765
tac	ggt	tct	gat	gcc	gat	gtg	atg	ttt	gta	tgc	gag	ccg	gta	gcc	ggt		2352
Tyr	Gly	Ser	Asp	Ala	Asp	Val	Met	Phe	Val	Cys	Glu	Pro	Val	Ala	Gly		
																770	775
																780	780
gtg	gaa	gag	cat	gag	gcc	gtc	aca	tgg	tct	att	gcg	atc	tgt	gat	tcc		2400
Val	Glu	Glu	His	Glu	Ala	Val	Thr	Trp	Ser	Ile	Ala	Ile	Cys	Asp	Ser		
																785	790
																795	800
atg	cgg	tcg	agg	ctt	gcg	cag	cct	tcc	ggt	gat	cca	cct	ttg	gag	gtg		2448
Met	Arg	Ser	Arg	Leu	Ala	Gln	Pro	Ser	Gly	Asp	Pro	Pro	Leu	Glu	Val		
																805	810
																815	815
gat	ctg	ggg	ctg	cgt	cct	gaa	ggg	aga	tct	ggt	gcg	att	gtg	cgc	acc		2496
Asp	Leu	Gly	Leu	Arg	Pro	Glu	Gly	Arg	Ser	Gly	Ala	Ile	Val	Arg	Thr		
																820	825
																830	830
gtt	gat	tcc	tat	gtg	aag	tac	tac	gaa	aag	tgg	ggt	gaa	act	tgg	gag		2544
Val	Asp	Ser	Tyr	Val	Lys	Tyr	Tyr	Glu	Lys	Trp	Gly	Glu	Thr	Trp	Glu		
																835	840
																845	845
att	cag	gcg	ctg	ctg	agg	gct	gcg	tgg	gtt	gct	ggt	gat	cgt	gag	ctg		2592
Ile	Gln	Ala	Leu	Leu	Arg	Ala	Ala	Trp	Val	Ala	Gly	Asp	Arg	Glu	Leu		
																850	855
																860	860
ggc	att	aag	tcc	ttg	gag	tcg	att	gat	cgt	tcc	cgc	tac	cca	gtt	gac		2640
Gly	Ile	Lys	Phe	Leu	Glu	Ser	Ile	Asp	Arg	Phe	Arg	Tyr	Pro	Val	Asp		
																865	870
																875	880
ggg	gca	acg	cag	gcg	cag	ctt	cgt	gaa	gtt	cgt	cga	att	aag	gcg	agg		2688
Gly	Ala	Thr	Gln	Ala	Gln	Leu	Arg	Glu	Val	Arg	Arg	Ile	Lys	Ala	Arg		
																885	890
																890	895
gtg	gat	aat	gag	agg	ctt	ccg	cgc	ggg	gct	gat	cga	aat	acc	cat	acc		2736
Val	Asp	Asn	Glu	Arg	Leu	Pro	Arg	Gly	Ala	Asp	Arg	Asn	Thr	His	Thr		
																900	905
																910	910
aag	ctg	ggt	cg	gga	g	tta	act	gac	atc	gag	tgg	act	gtg	cag	ttg		2784
Lys	Leu	Gly	Arg	Gly	Ala	Leu	Thr	Asp	Ile	Glu	Trp	Thr	Val	Gln	Leu		
																915	920
																925	925
ttg	acc	atg	atg	cat	gct	cat	gag	att	ccg	gag	ctg	cac	aat	acg	tcg		2832

US-162

Leu	Thr	Met	Met	His	Ala	His	Glu	Ile	Pro	Glu	Leu	His	Asn	Thr	Ser	
930				935						940						
acg	ttg	gaa	gtt	ctt	gaa	gtg	ctg	gaa	aag	cat	cag	att	att	aac	cct	2880
Thr	Leu	Glu	Val	Leu	Glu	Val	Leu	Glu	Lys	His	Gln	Ile	Ile	Asn	Pro	
945				950					955						960	
gtg	cag	gtg	cag	acg	ctt	cgg	gaa	gcf	tgg	ctg	acg	gca	acg	gct	gct	2928
Val	Gln	Val	Gln	Thr	Leu	Arg	Glu	Ala	Trp	Leu	Thr	Ala	Thr	Ala	Ala	
															975	
965									970							
agg	aat	gcf	ctt	gtg	ctg	gtc	agg	ggt	aag	aga	tta	gat	cag	tta	cct	2976
Arg	Asn	Ala	Leu	Val	Leu	Val	Arg	Gly	Lys	Arg	Leu	Asp	Gln	Leu	Pro	
									985						990	
980																
act	cct	ggt	ccg	cac	ctt	gcf	cag	gtg	gct	ggt	gcf	tct	ggt	tgg	gat	3024
Thr	Pro	Gly	Pro	His	Leu	Ala	Gln	Val	Ala	Gly	Ala	Ser	Gly	Trp	Asp	
									995						1005	
cca	aat	gag	tac	cag	gag	tat	ttg	gaa	aac	tat	ctg	aaa	gtg	acc	agg	3072
Pro	Asn	Glu	Tyr	Gln	Glu	Tyr	Leu	Glu	Asn	Tyr	Leu	Lys	Val	Thr	Arg	
									1010						1020	
aag	agt	cgt	cag	gtt	gtt	gat	gaa	gtc	tcc	tgg	ggt	gtg	gac	tct	atg	3120
Lys	Ser	Arg	Gln	Val	Val	Asp	Glu	Val	Phe	Trp	Gly	Val	Asp	Ser	Met	
									1025						1040	
gag	caa	cgt	gag	ttt	tag											3138
Glu	Gln	Arg	Glu	Phe												
				1045												

<210> 18

<211> 1045

<212> PRT

<213> Brevibacterium lactofermentum

<400> 18

Met	Ser	Gly	Pro	Leu	Arg	Ser	Glu	Arg	Lys	Val	Val	Gly	Phe	Val	Arg	
1				5					10					15		
Asp	Pro	Leu	Pro	Lys	Val	Gly	Ser	Leu	Ser	Leu	Lys	Ser	Glu	His	Ala	
									20					30		
Gln	Ala	Asp	Leu	Glu	His	Leu	Gly	Trp	Arg	Asn	Val	Glu	Ser	Leu	Asp	
									35					45		
Leu	Leu	Trp	Gly	Leu	Ser	Gly	Ala	Gly	Asp	Pro	Asp	Val	Ala	Leu	Asn	
									50					60		
Leu	Leu	Ile	Arg	Leu	Tyr	Gln	Ala	Leu	Glu	Ala	Ile	Gly	Glu	Asp	Ala	
									65					80		
Arg	Asn	Glu	Leu	Asp	Gln	Glu	Ile	Arg	Gln	Asp	Glu	Glu	Leu	Arg	Val	
									85					95		
Arg	Leu	Phe	Ala	Leu	Leu	Gly	Gly	Ser	Ser	Ala	Val	Gly	Asp	His	Leu	
									100					110		
val	Ala	Asn	Pro	Leu	Gln	Trp	Lys	Leu	Leu	Lys	Leu	Asp	Ala	Pro	Ser	
									115					125		
Arg	Glu	Glu	Met	Phe	Gln	Ala	Leu	Leu	Glu	Ser	Val	Lys	Ala	Gln	Pro	
									130					140		
Ala	Val	Leu	Glu	Val	Glu	Asp	Phe	Ser	Asp	Ala	His	Asn	Ile	Ala	Arg	
									145					160		
Asp	Asp	Leu	Ser	Thr	Pro	Gly	Phe	Tyr	Thr	Ala	Ser	val	Thr	Gly	Pro	
									165					175		
Glu	Ala	Glu	Arg	Val	Leu	Lys	Trp	Thr	Tyr	Arg	Thr	Leu	Leu	Thr	Arg	
									180					190		
Ile	Ala	Ala	His	Asp	Leu	Ala	Gly	Thr	Tyr	Pro	Thr	Asp	Met	Arg	Arg	

US-162

Lys	Gly	Gly	Asp	Pro	Val	Pro	Phe	Ser	Thr	Val	Thr	Met	Gln	Leu	Ser	
195	200	205														
210	215	220														
Asp	Leu	Ala	Asp	Ala	Ala	Leu	Thr	Ala	Ala	Leu	Ala	Val	Ala	Ile	Ala	
225	230	235													240	
Asn	Val	Tyr	Gly	Glu	Lys	Pro	Val	Asp	Ser	Ala	Leu	Ser	Val	Ile	Ala	
															245	
Met	Gly	Lys	Cys	Gly	Ala	Gln	Glu	Leu	Asn	Tyr	Ile	Ser	Asp	Val	Asp	
															250	
260	265	270														
Val	Val	Phe	Val	Ala	Glu	Pro	Ala	Asn	Ser	Lys	Ser	Thr	Arg	Thr	Ala	
															275	
275	280	285														
Ala	Glu	Leu	Ile	Arg	Ile	Gly	Ser	Asn	Ser	Phe	Phe	Glu	Val	Asp	Ala	
															290	
															295	
															300	
Ala	Leu	Arg	Pro	Glu	Gly	Lys	Ser	Gly	Ala	Leu	Val	Arg	Ser	Leu	Asp	
															305	
															310	
Ser	His	Met	Ala	Tyr	Tyr	Lys	Arg	Trp	Ala	Glu	Thr	Trp	Glu	Phe	Gln	
															325	
															330	
Ala	Leu	Leu	Lys	Ala	Arg	Pro	Met	Thr	Gly	Asp	Ile	Asp	Leu	Gly	Gln	
															340	
															345	
Ser	Tyr	Val	Asp	Ala	Leu	Ser	Pro	Leu	Ile	Trp	Ala	Ala	Ser	Gln	Arg	
															355	
															360	
Glu	Ser	Phe	Val	Thr	Asp	Val	Gln	Ala	Met	Arg	Arg	Arg	Arg	Val	Leu	Asp
															370	
															375	
															380	
Asn	Val	Pro	Glu	Asp	Leu	Arg	Asp	Arg	Glu	Leu	Lys	Leu	Gly	Arg	Gly	
															385	
															390	
Gly	Leu	Arg	Asp	Val	Glu	Phe	Ala	Val	Gln	Leu	Leu	Gln	Met	Val	His	
															405	
Gly	Arg	Ile	Asp	Glu	Thr	Leu	Arg	Val	Arg	Ser	Thr	Val	Asn	Ala	Leu	
															420	
															425	
His	Val	Leu	Val	Asp	Gln	Gly	Tyr	Val	Gly	Arg	Glu	Asp	Gly	His	Asn	
															435	
															440	
Leu	Ile	Glu	Ser	Tyr	Glu	Phe	Leu	Arg	Leu	Leu	Glu	His	Arg	Leu	Gln	
															450	
															455	
Leu	Glu	Arg	Ile	Lys	Arg	Thr	His	Leu	Leu	Pro	Lys	Pro	Asp	Asp	Arg	
															465	
															470	
Met	Asn	Met	Arg	Trp	Leu	Ala	Arg	Ala	Ser	Gly	Phe	Thr	Gly	Ser	Met	
															485	
															490	
Glu	Gln	Ser	Ser	Ala	Lys	Ala	Met	Glu	Arg	His	Leu	Arg	Lys	Val	Arg	
															500	
															505	
Leu	Gln	Ile	Gln	Ser	Leu	His	Ser	Gln	Leu	Phe	Tyr	Arg	Pro	Leu	Leu	
															515	
															520	
Asn	Ser	Val	val	Asn	Leu	Ser	Ala	Asp	Ala	Ile	Arg	Leu	Ser	Pro	Asp	
															530	
															535	
Ala	Ala	Lys	Leu	Gln	Leu	Gly	Ala	Leu	Gly	Tyr	Leu	His	Pro	Ser	Arg	
															545	
															550	
Ala	Tyr	Glu	His	Leu	Thr	Ala	Leu	Ala	Ser	Gly	Ala	Ser	Arg	Lys	Ala	
															565	
															570	
Lys	Ile	Gln	Ala	Met	Leu	Leu	Pro	Thr	Leu	Met	Glu	Trp	Leu	Ser	Gln	
															580	
															585	
Thr	Ala	Glu	Pro	Asp	Ala	Gly	Leu	Leu	Asn	Tyr	Arg	Lys	Leu	Ser	Asp	
															595	
															600	
Ala	Ser	Tyr	Asp	Arg	Ser	Trp	Phe	Leu	Arg	Met	Leu	Arg	Asp	Glu	Gly	
															610	
															615	
Val	Val	Gly	Gln	Arg	Leu	Met	Arg	Ile	Leu	Gly	Asn	Ser	Pro	Tyr	Ile	
															625	
															630	
															635	
															640	

US-162

Ser Glu Leu Ile Ile Ser Thr Pro Asp Phe Val Lys Gln Leu Gly Asp
 645 650 655
 Ala Ala Ser Gly Pro Lys Leu Leu Ala Thr Ala Pro Thr Gln Val Val
 660 665 670
 Lys Ala Ile Lys Ala Thr Val Ser Arg His Glu Ser Pro Asp Arg Ala
 675 680 685
 Ile Gln Ala Ala Arg Ser Leu Arg Arg Gln Glu Leu Ala Arg Ile Ala
 690 695 700
 Ser Ala Asp Leu Leu Asn Met Leu Thr Val Gln Glu Val Cys Gln Ser
 705 710 715 720
 Leu Ser Leu Val Trp Asp Ala Val Leu Asp Ala Ala Leu Asp Ala Glu
 725 730 735
 Ile Arg Ala Ala Leu Asn Asp Pro Gln Lys Pro Asp Gln Pro Leu Ala
 740 745 750
 Asn Ile Ser Val Ile Gly Met Gly Arg Leu Gly Gly Ala Glu Leu Gly
 755 760 765
 Tyr Gly Ser Asp Ala Asp Val Met Phe Val Cys Glu Pro Val Ala Gly
 770 775 780
 Val Glu Glu His Glu Ala Val Thr Trp Ser Ile Ala Ile Cys Asp Ser
 785 790 795 800
 Met Arg Ser Arg Leu Ala Gln Pro Ser Gly Asp Pro Pro Leu Glu Val
 805 810 815
 Asp Leu Gly Leu Arg Pro Glu Gly Arg Ser Gly Ala Ile Val Arg Thr
 820 825 830
 Val Asp Ser Tyr Val Lys Tyr Glu Lys Trp Gly Glu Thr Trp Glu
 835 840 845
 Ile Gln Ala Leu Leu Arg Ala Ala Trp Val Ala Gly Asp Arg Glu Leu
 850 855 860
 Gly Ile Lys Phe Leu Glu Ser Ile Asp Arg Phe Arg Tyr Pro Val Asp
 865 870 875 880
 Gly Ala Thr Gln Ala Gln Leu Arg Glu Val Arg Arg Ile Lys Ala Arg
 885 890 895
 Val Asp Asn Glu Arg Leu Pro Arg Gly Ala Asp Arg Asn Thr His Thr
 900 905 910
 Lys Leu Gly Arg Gly Ala Leu Thr Asp Ile Glu Trp Thr Val Gln Leu
 915 920 925
 Leu Thr Met Met His Ala His Glu Ile Pro Glu Leu His Asn Thr Ser
 930 935 940
 Thr Leu Glu Val Leu Glu Val Leu Glu Lys His Gln Ile Ile Asn Pro
 945 950 955 960
 Val Gln Val Gln Thr Leu Arg Glu Ala Trp Leu Thr Ala Thr Ala Ala
 965 970 975
 Arg Asn Ala Leu Val Leu Val Arg Gly Lys Arg Leu Asp Gln Leu Pro
 980 985 990
 Thr Pro Gly Pro His Leu Ala Gln Val Ala Gly Ala Ser Gly Trp Asp
 995 1000 1005
 Pro Asn Glu Tyr Gln Glu Tyr Leu Glu Asn Tyr Leu Lys Val Thr Arg
 1010 1015 1020
 Lys Ser Arg Gln Val Val Asp Glu Val Phe Trp Gly Val Asp Ser Met
 1025 1030 1035 1040
 Glu Gln Arg Glu Phe
 1045

<210> 19
 <211> 1434

US-162

<212> DNA
 <213> *Brevibacterium lactofermentum*
 <220>
 <221> CDS
 <222> (1)..(1434)

<400> 19		
gtg gcg ttt gaa acc ccg gaa gaa att gtc aag ttc atc aag gat gaa	48	
Val Ala Phe Glu Thr Pro Glu Glu Ile Val Lys Phe Ile Lys Asp Glu		
1 5 10 15		
aac gtc gag ttc gtt gac gtt cga ttc acc gac ctt ccc ggc acc gag	96	
Asn Val Glu Phe Val Asp Val Arg Phe Thr Asp Leu Pro Gly Thr Glu		
20 25 30		
cag cac ttc agc atc cca gct gcc agc ttc gat gca gat aca gtc gaa	144	
Gln His Phe Ser Ile Pro Ala Ala Ser Phe Asp Ala Asp Thr Val Glu		
35 40 45		
gaa ggt ctc gca ttc gac gga tcc tcg atc cgt ggc ttc acc acg atc	192	
Glu Gly Leu Ala Phe Asp Gly Ser Ser Ile Arg Gly Phe Thr Thr Ile		
50 55 60		
gac gaa tct gac atg aat ctc ctc cca gac ctc gga acg gcc acc ctt	240	
Asp Glu Ser Asp Met Asn Leu Leu Pro Asp Leu Gly Thr Ala Thr Leu		
65 70 75 80		
gat cca ttc cgc aag gca aag acc ctg aac gtt aag ttc ttc gtt cac	288	
Asp Pro Phe Arg Lys Ala Lys Thr Leu Asn Val Lys Phe Phe Val His		
85 90 95		
gat cct ttc acc cgc gag gca ttc tcc cgc gac cca cgc aac gta gca	336	
Asp Pro Phe Thr Arg Glu Ala Phe Ser Arg Asp Pro Arg Asn Val Ala		
100 105 110		
cgc aag gca gag cag tac ctg gca tcc acc ggc att gca gac acc tgc	384	
Arg Lys Ala Glu Gln Tyr Leu Ala Ser Thr Gly Ile Ala Asp Thr Cys		
115 120 125		
aac ttc ggc gcc gag gct gag ttc tac ctc ttc gac tcc gtt cgc tac	432	
Asn Phe Gly Ala Glu Ala Glu Phe Tyr Leu Phe Asp Ser Val Arg Tyr		
130 135 140		
tcc acc gag atg aac tcc ggc ttc tac gaa gta gat acc gaa gaa ggc	480	
Ser Thr Glu Met Asn Ser Gly Phe Tyr Glu Val Asp Thr Glu Glu Gly		
145 150 155 160		
tgg tgg aac cgt ggc aag gaa acc aac ctc gac gga acc cca aac ctg	528	
Trp Trp Asn Arg Gly Lys Glu Thr Asn Leu Asp Gly Thr Pro Asn Leu		
165 170 175		
ggc gca aag aac cgc gtc aag ggt ggc tac ttc cca gta gca cca tac	576	
Gly Ala Lys Asn Arg Val Lys Gly Gly Tyr Phe Pro Val Ala Pro Tyr		
180 185 190		
gac caa acc gtt gac gtg cgc gat gac atg gtt cgc aac ctc gca gct	624	
Asp Gln Thr Val Asp Val Arg Asp Asp Met Val Arg Asn Leu Ala Ala		
195 200 205		
tcc ggc ttc gct ctt gag cgt ttc cac cac gaa gtc ggt ggc gga cag	672	
Ser Gly Phe Ala Leu Glu Arg Phe His His Glu Val Gly Gly Gly Gln		
210 215 220		
cag gaa atc aac tac cgc ttc aac acc atg ctc cac gcg gca gat gat	720	
Gln Glu Ile Asn Tyr Arg Phe Asn Thr Met Leu His Ala Ala Asp Asp		
225 230 235 240		
atc cag acc ttc aag tac atc atc aag aac acc gct cgc ctc cac ggc	768	
Ile Gln Thr Phe Lys Tyr Ile Ile Lys Asn Thr Ala Arg Leu His Gly		

US-162

aag gct gca acc ttc atg cct aag cca	245	ctg gct ggc gac aac ggt tcc	250	255		816
Lys Ala Ala Thr Phe Met Pro Lys		Pro Leu Ala Gly Asp Asn Gly Ser				
260	265	270				
ggc atg cac gct cac cag tcc ctc tgg aag gac ggc aag cca ctc ttc						864
Gly Met His Ala His Gln Ser Leu Trp Lys Asp Gly Lys Pro Leu Phe						
275	280	285				
cac gat gag tcc ggc tac gca ggc ctg tcc gac atc gcc cgc tac tac						912
His Asp Glu Ser Gly Tyr Ala Gly Leu Ser Asp Ile Ala Arg Tyr Tyr						
290	295	300				
atc ggc ggc atc ctg cac cac gca ggc gct gtt ctg gcg ttc acc aac						960
Ile Gly Ile Leu His His Ala Gly Ala Val Leu Ala Phe Thr Asn						
305	310	315	320			
gca acc ctg aac tcc tac cac cgt ctg gtt cca ggc ttc gag gct cca						1008
Ala Thr Leu Asn Ser Tyr His Arg Leu Val Pro Gly Phe Glu Ala Pro						
325	330	335				
atc aac ctg gtg tac tca cag cgc aac cgt tcc gct gtc cgt atc						1056
Ile Asn Leu Val Tyr Ser Gln Arg Asn Arg Ser Ala Ala Val Arg Ile						
340	345	350				
cca atc acc gga tcc aac cca aag gca aag cgc atc gaa ttc cgc gct						1104
Pro Ile Thr Gly Ser Asn Pro Lys Ala Lys Arg Ile Glu Phe Arg Ala						
355	360	365				
cca gac cca tca ggc aac cca tac ctg ggc ttc gca gcg atg atg atg						1152
Pro Asp Pro Ser Gly Asn Pro Tyr Leu Gly Phe Ala Ala Met Met Met						
370	375	380				
gcc ggc ctc gac ggc atc aag aac cgc atc gag cca cac gct cca gtg						1200
Ala Gly Leu Asp Gly Ile Lys Asn Arg Ile Glu Pro His Ala Pro Val						
385	390	395	400			
gac aag gac ctc tac gaa ctg cca cca gag gaa gct gca tcc att cca						1248
Asp Lys Asp Leu Tyr Glu Leu Pro Pro Glu Glu Ala Ala Ser Ile Pro						
405	410	415				
cag gca cca acc tcc ctg gaa gca tcc ctg aag gca ctg cag gaa gac						1296
Gln Ala Pro Thr Ser Leu Glu Ala Ser Leu Lys Ala Leu Gln Glu Asp						
420	425	430				
acc gac ttc ctc acc gag tct gac gtc ttc acc gag gat ctc atc gag						1344
Thr Asp Phe Leu Thr Glu Ser Asp Val Phe Thr Glu Asp Leu Ile Glu						
435	440	445				
gcg tac atc cag tac aag tac gac aac gag atc tcc cca gtt cgc ctg						1392
Ala Tyr Ile Gln Tyr Lys Tyr Asp Asn Glu Ile Ser Pro Val Arg Leu						
450	455	460				
cgc cca acc ccg cag gaa ttc gaa ttg tac ttc gac tgc taa						1434
Arg Pro Thr Pro Gln Glu Phe Glu Leu Tyr Phe Asp Ala Asp Cys						
465	470	475				

<210> 20
<211> 477
<212> PRT
<213> *Brevibacterium lactofermentum*

<400> 20
Val Ala Phe Glu Thr Pro Glu Glu Ile Val Lys Phe Ile Lys Asp Glu
1 5 10 15
Asn Val Glu Phe Val Asp Val Arg Phe Thr Asp Leu Pro Gly Thr Glu
20 25 30
Gln His Phe Ser Ile Pro Ala Ala Ser Phe Asp Ala Asp Thr Val Glu

US-162

Glu	Gly	Leu	Ala	Phe	Asp	Gly	Ser	Ser	Ile	Arg	Gly	Phe	Thr	Thr	Ile
35						40					45				
50						55					60				
Asp	Glu	Ser	Asp	Met	Asn	Leu	Leu	Pro	Asp	Leu	Gly	Thr	Ala	Thr	Leu
65						70					75				80
Asp	Pro	Phe	Arg	Lys	Ala	Lys	Thr	Leu	Asn	Val	Lys	Phe	Phe	Val	His
						85					90				95
Asp	Pro	Phe	Thr	Arg	Glu	Ala	Phe	Ser	Arg	Asp	Pro	Arg	Asn	Val	Ala
						100					105				110
Arg	Lys	Ala	Glu	Gln	Tyr	Leu	Ala	Ser	Thr	Gly	Ile	Ala	Asp	Thr	Cys
						115					120				125
Asn	Phe	Gly	Ala	Glu	Ala	Glu	Phe	Tyr	Leu	Phe	Asp	Ser	Val	Arg	Tyr
						130					135				140
Ser	Thr	Glu	Met	Asn	Ser	Gly	Phe	Tyr	Glu	Val	Asp	Thr	Glu	Glu	Gly
145						150					155				160
Trp	Trp	Asn	Arg	Gly	Lys	Glu	Thr	Asn	Leu	Asp	Gly	Thr	Pro	Asn	Leu
						165					170				175
Gly	Ala	Lys	Asn	Arg	Val	Lys	Gly	Gly	Tyr	Phe	Pro	Val	Ala	Pro	Tyr
						180					185				190
Asp	Gln	Thr	Val	Asp	Val	Arg	Asp	Asp	Met	Val	Arg	Asn	Leu	Ala	Ala
						195					200				205
Ser	Gly	Phe	Ala	Leu	Glu	Arg	Phe	His	His	Glu	Val	Gly	Gly	Gly	Gln
						210					215				220
Gln	Glu	Ile	Asn	Tyr	Arg	Phe	Asn	Thr	Met	Leu	His	Ala	Ala	Asp	Asp
225						230					235				240
Ile	Gln	Thr	Phe	Lys	Tyr	Ile	Ile	Lys	Asn	Thr	Ala	Arg	Leu	His	Gly
						245					250				255
Lys	Ala	Ala	Thr	Phe	Met	Pro	Lys	Pro	Leu	Ala	Gly	Asp	Asn	Gly	Ser
						260					265				270
Gly	Met	His	Ala	His	Gln	Ser	Leu	Trp	Lys	Asp	Gly	Lys	Pro	Leu	Phe
						275					280				285
His	Asp	Glu	Ser	Gly	Tyr	Ala	Gly	Leu	Ser	Asp	Ile	Ala	Arg	Tyr	Tyr
						290					295				300
Ile	Gly	Gly	Ile	Leu	His	His	Ala	Gly	Ala	Val	Leu	Ala	Phe	Thr	Asn
						305					310				320
Ala	Thr	Leu	Asn	Ser	Tyr	His	Arg	Leu	Val	Pro	Gly	Phe	Glu	Ala	Pro
						325					330				335
Ile	Asn	Leu	Val	Tyr	Ser	Gln	Arg	Asn	Arg	Ser	Ala	Ala	Val	Arg	Ile
						340					345				350
Pro	Ile	Thr	Gly	Ser	Asn	Pro	Lys	Ala	Lys	Arg	Ile	Glu	Phe	Arg	Ala
						355					360				365
Pro	Asp	Pro	Ser	Gly	Asn	Pro	Tyr	Leu	Gly	Phe	Ala	Ala	Met	Met	Met
						370					375				380
Ala	Gly	Leu	Asp	Gly	Ile	Lys	Asn	Arg	Ile	Glu	Pro	His	Ala	Pro	Val
						385					390				400
Asp	Lys	Asp	Leu	Tyr	Glu	Leu	Pro	Pro	Glu	Glu	Ala	Ala	Ser	Ile	Pro
						405					410				415
Gln	Ala	Pro	Thr	Ser	Leu	Glu	Ala	Ser	Leu	Lys	Ala	Leu	Gln	Glu	Asp
						420					425				430
Thr	Asp	Phe	Leu	Thr	Glu	Ser	Asp	Val	Phe	Thr	Glu	Asp	Leu	Ile	Glu
						435					440				445
Ala	Tyr	Ile	Gln	Tyr	Lys	Tyr	Asp	Asn	Glu	Ile	Ser	Pro	Val	Arg	Leu
						450					455				460
Arg	Pro	Thr	Pro	Gln	Glu	Phe	Glu	Leu	Tyr	Phe	Asp	Cys			
						465					470				475

US-162

<210> 21
 <211> 672
 <212> DNA
 <213> *Brevibacterium lactofermentum*

<220>
 <221> CDS
 <222> (1)..(669)

<400> 21	48
atg gca gga gca gtg gga cgc ccc cg ^g aga tca gct ccg cga cg ^g gca	
Met Ala Gly Ala Val Gly Arg Pro Arg Arg Ser Ala Pro Arg Arg Ala	
1 5 10 15	
ggc aag aat cct cgc gag gag att ctt gac gcc tct gct gag ctt ttc	
Gly Lys Asn Pro Arg Glu Glu Ile Leu Asp Ala Ser Ala Glu Leu Phe	
20 25 30	
acc cat caa ggc ttc gca aca acc tcc acg cat caa atc gct gat gcc	
Thr His Gln Gly Phe Ala Thr Thr Ser Thr His Gln Ile Ala Asp Ala	
35 40 45	
gtg gga atc cgc caa gcc tcg ctg tat tat cac ttc ccg tct aag acg	
Val Gly Ile Arg Gln Ala Ser Leu Tyr Tyr His Phe Pro Ser Lys Thr	
50 55 60	
gaa atc ttc ctc acc ctc ctg aaa tct acc gtc gag ccg tcc act gtg	
Glu Ile Phe Leu Thr Leu Lys Ser Thr Val Glu Pro Ser Thr Val	
65 70 75 80	
ctc gcc gaa gac tta agc atc ctg gat gca gga cct gag atg cgc ctc	
Leu Ala Glu Asp Leu Ser Ile Leu Asp Ala Gly Pro Glu Met Arg Leu	
85 90 95	
tgg gca atc gtt gcc tcc gaa gtg cgt ctg ctg ctg tcc acc aag tgg	
Trp Ala Ile Val Ala Ser Glu Val Arg Leu Leu Leu Ser Thr Lys Trp	
100 105 110	
aac gtc ggt cgc ctg tac caa ctc ccc atc gtt ggt tct gaa gag ttc	
Asn Val Gly Arg Leu Tyr Gln Leu Pro Ile Val Gly Ser Glu Glu Phe	
115 120 125	
gcc gag tac cac agc cag cgc gaa gcc ctc acc aac atc ttc cgc gac	
Ala Glu Tyr His Ser Gln Arg Glu Ala Leu Thr Asn Ile Phe Arg Asp	
130 135 140	
ctc gcc acc gaa atc gtc ggt gac gac ccc cgc gca gaa ctc ccc ttc	
Leu Ala Thr Glu Ile Val Gly Asp Asp Pro Arg Ala Glu Leu Pro Phe	
145 150 155 160	
cac atc acc atg tcg gtg atc gaa atg cgt cgc aac gac ggc aag att	
His Ile Thr Met Ser Val Ile Glu Met Arg Arg Asn Asp Gly Lys Ile	
165 170 175	
cca agc ccg ctt tcc gca gac agc ctc ccg gag acc gca att atg ctt	
Pro Ser Pro Leu Ser Ala Asp Ser Leu Pro Glu Thr Ala Ile Met Leu	
180 185 190	
gcc gac gcc tcc ctc gcc gtc ctc ggc gcg tcg ctg ccc gcc gac cg ^g	
Ala Asp Ala Ser Leu Ala Val Leu Gly Ala Ser Leu Pro Ala Asp Arg	
195 200 205	
gtc gaa aaa acg ctt gaa cta atc aag cag gct gac ggc aaa taa cca	
Val Glu Lys Thr Leu Glu Leu Ile Lys Gln Ala Asp Ala Lys	
210 215 220	

<210> 22

US-162

<211> 222

<212> PRT

<213> Brevibacterium lactofermentum

<400> 22

Met Ala Gly Ala Val Gly Arg Pro Arg Arg Ser Ala Pro Arg Arg Ala
 1 5 10 15
 Gly Lys Asn Pro Arg Glu Glu Ile Leu Asp Ala Ser Ala Glu Leu Phe
 20 25 30
 Thr His Gln Gly Phe Ala Thr Thr Ser Thr His Gln Ile Ala Asp Ala
 35 40 45
 Val Gly Ile Arg Gln Ala Ser Leu Tyr Tyr His Phe Pro Ser Lys Thr
 50 55 60
 Glu Ile Phe Leu Thr Leu Leu Lys Ser Thr Val Glu Pro Ser Thr Val
 65 70 75 80
 Leu Ala Glu Asp Leu Ser Ile Leu Asp Ala Gly Pro Glu Met Arg Leu
 85 90 95
 Trp Ala Ile Val Ala Ser Glu Val Arg Leu Leu Leu Ser Thr Lys Trp
 100 105 110
 Asn Val Gly Arg Leu Tyr Gln Leu Pro Ile Val Gly Ser Glu Glu Phe
 115 120 125
 Ala Glu Tyr His Ser Gln Arg Glu Ala Leu Thr Asn Ile Phe Arg Asp
 130 135 140
 Leu Ala Thr Glu Ile Val Gly Asp Asp Pro Arg Ala Glu Leu Pro Phe
 145 150 155 160
 His Ile Thr Met Ser Val Ile Glu Met Arg Arg Asn Asp Gly Lys Ile
 165 170 175
 Pro Ser Pro Leu Ser Ala Asp Ser Leu Pro Glu Thr Ala Ile Met Leu
 180 185 190
 Ala Asp Ala Ser Leu Ala Val Leu Gly Ala Ser Leu Pro Ala Asp Arg
 195 200 205
 Val Glu Lys Thr Leu Glu Leu Ile Lys Gln Ala Asp Ala Lys
 210 215 220

<210> 23

<211> 2076

<212> DNA

<213> Brevibacterium lactofermentum

<220>

<221> CDS

<222> (1)..(2076)

<400> 23

atg aat aat cca gcc cag ctg cgc caa gat act gaa aag gaa gtc ctg	48
Met Asn Asn Pro Ala Gln Leu Arg Gln Asp Thr Glu Lys Glu Val Leu	
1 5 10 15	
gcg ttg ctg ggc tct ttg gtt tta ccc gcc ggc acc gcg ctt gcc gcc	96
Ala Leu Leu Gly Ser Leu Val Leu Pro Ala Gly Thr Ala Leu Ala Ala	
20 25 30	
acc gga tct ttg gcc agg tcc gaa ctc acg ccg tat tcc gat ttg gac	144
Thr Gly Ser Leu Ala Arg Ser Glu Leu Thr Pro Tyr Ser Asp Leu Asp	
35 40 45	
ctc att ttg atc cat cca cca ggg gca acc ccg gat ggc gtg gag gat	192
Leu Ile Leu Ile His Pro Pro Gly Ala Thr Pro Asp Gly Val Glu Asp	

US-162

US-162

atg	gat	cgc	cac	gga	ttg	tgg	tcg	cgt	ttt	gtt	cca	gaa	tgg	gac	cgc		1104
Met	Asp	Arg	His	Gly	Leu	Trp	Ser	Arg	Phe	Val	Pro	Glu	Trp	Asp	Arg		
355					360					365							
atc	aaa	ggg	ctt	atg	ccc	cgt	gaa	ccc	agc	cat	att	tcc	acc	atc	gat		1152
Ile	Lys	Gly	Leu	Met	Pro	Arg	Glu	Pro	Ser	His	Ile	Ser	Thr	Ile	Asp		
370					375					380							
gaa	cat	agt	ctg	aac	act	gtt	gca	gga	tgt	gcg	cta	gaa	act	gtg	acc		1200
Glu	His	Ser	Leu	Asn	Thr	Val	Ala	Gly	Cys	Ala	Leu	Glu	Thr	Val	Thr		
385					390					395					400		
gtc	gcf	cgc	ccc	gat	ctt	tta	gtt	ttg	gga	gcc	ttg	tac	cac	gac	att		1248
Val	Ala	Arg	Pro	Asp	Leu	Leu	Val	Leu	Gly	Ala	Leu	Tyr	His	Asp	Ile		
											405	410	415				
ggc	aag	ggc	ttc	ccg	cgt	cca	cac	gaa	caa	gta	ggt	gca	gag	atg	gtg		1296
Gly	Lys	Gly	Phe	Pro	Arg	Pro	His	Glu	Gln	Val	Gly	Ala	Glu	Met	Val		
											420	425	430				
gcf	agg	gcc	gcf	agc	cgc	atg	ggg	ttg	aac	ctt	cgc	gat	cgt	gcc	agc		1344
Ala	Arg	Ala	Ala	Ser	Arg	Met	Gly	Leu	Asn	Leu	Arg	Asp	Arg	Ala	Ser		
											435	440	445				
gtg	caa	acg	ctg	gtc	gcc	gag	cac	acc	gcf	gtg	gcc	aaa	atc	gcc	gcf		1392
Val	Gln	Thr	Leu	Val	Ala	Glu	His	Thr	Ala	Val	Ala	Lys	Ile	Ala	Ala		
											450	455	460				
cgf	ctt	gat	ccc	tcc	tcg	gag	ggc	gcc	gtc	gat	aag	ctg	ctt	gat	gct		1440
Arg	Leu	Asp	Pro	Ser	Ser	Glu	Gly	Ala	Val	Asp	Lys	Leu	Leu	Asp	Ala		
											465	470	475	480			
gtt	agg	tat	gac	ctg	gtg	aca	ttg	aat	ctg	ctt	gag	gtg	cta	aca	gaa		1488
Val	Arg	Tyr	Asp	Leu	Val	Thr	Leu	Asn	Leu	Leu	Glu	Val	Leu	Thr	Glu		
											485	490	495				
gct	gat	gcf	aaa	gcc	acg	ggg	cct	ggc	gta	tgg	acg	gcf	cgt	ttg	gag		1536
Ala	Asp	Ala	Lys	Ala	Thr	Gly	Pro	Gly	Val	Trp	Thr	Ala	Arg	Leu	Glu		
											500	505	510				
cat	gcf	ctg	cgf	att	gtg	tgc	aag	cgt	gcf	cgt	gat	cgc	ctc	acc	gat		1584
His	Ala	Leu	Arg	Ile	Val	Cys	Lys	Arg	Ala	Arg	Asp	Arg	Leu	Thr	Asp		
											515	520	525				
att	cgf	ccg	gtt	gcf	ccg	atg	att	gcf	ccg	cgt	agc	gaa	att	ggt	ttg		1632
Ile	Arg	Pro	Val	Ala	Pro	Met	Ile	Ala	Pro	Arg	Ser	Glu	Ile	Gly	Leu		
											530	535	540				
gtg	gaa	cgf	gat	ggc	gtg	tcc	aca	gtg	caa	tgg	cac	ggc	gaa	gac	tta		1680
Val	Glu	Arg	Asp	Gly	Val	Phe	Thr	Val	Gln	Trp	His	Gly	Glu	Asp	Leu		
											545	550	555	560			
cat	cgf	att	ctt	ggc	gta	att	tat	gcc	aaa	gga	tgg	aca	atc	acc	gcf		1728
His	Arg	Ile	Leu	Gly	Val	Ile	Tyr	Ala	Lys	Gly	Trp	Thr	Ile	Thr	Ala		
											565	570	575				
gcf	cgf	atg	ctg	gcc	aat	ggt	caa	tgg	agt	gcf	gaa	ttt	gat	gtc	cgc		1776
Ala	Arg	Met	Leu	Ala	Asn	Gly	Gln	Trp	Ser	Ala	Glu	Phe	Asp	Val	Arg		
											580	585	590				
gca	aac	ggc	ccc	caa	gat	ttt	gat	ccg	cag	cat	tcc	ctg	cag	gca	tat		1824
Ala	Asn	Gly	Pro	Gln	Asp	Phe	Asp	Pro	Gln	His	Phe	Leu	Gln	Ala	Tyr		
											595	600	605	610			
caa	tcc	ggf	gtg	ttt	tcc	gag	gtt	ccc	att	cca	gca	cct	ggg	ata	aca		1872
Gln	Ser	Gly	Val	Phe	Ser	Glu	Val	Pro	Ile	Pro	Ala	Pro	Gly	Ile	Thr		
											610	615	620				
gcc	aca	ttt	tgg	cac	ggg	aac	act	tta	gaa	gtg	cgc	act	gag	ctt	cgc		1920
Ala	Thr	Phe	Trp	His	Gly	Asn	Thr	Leu	Glu	Val	Arg	Thr	Glu	Leu	Arg		
											625	630	635	640			
aca	gga	gct	att	ttt	gcc	ctg	ctc	aga	aca	ttg	ccc	gat	gcc	ctc	tgg		1968

US-162

Thr Gly Ala Ile Phe Ala Leu Leu Arg Thr Leu Pro Asp Ala Leu Trp			
645	650	655	
atc aac gct gtg acc cgc ggt gcg acc ctg att atc cag gca gca ctg			2016
Ile Asn Ala Val Thr Arg Gly Ala Thr Leu Ile Ile Gln Ala Ala Leu			
660	665	670	
aag ccc ggc ttc gat cga gca acg gtg gaa cgc tcc gta gtc agg tcg			2064
Lys Pro Gly Phe Asp Arg Ala Thr Val Glu Arg Ser Val Val Arg Ser			
675	680	685	
ttg gca ggt agc			2076
Leu Ala Gly Ser			
690			

<210> 24

<211> 692

<212> PRT

<213> *Brevibacterium lactofermentum*

<400> 24

Met Asn Asn Pro Ala Gln Leu Arg Gln Asp Thr Glu Lys Glu Val Leu			
1	5	10	15
Ala Leu Leu Gly Ser Leu Val Leu Pro Ala Gly Thr Ala Leu Ala Ala			
20	25	30	
Thr Gly Ser Leu Ala Arg Ser Glu Leu Thr Pro Tyr Ser Asp Leu Asp			
35	40	45	
Leu Ile Leu Ile His Pro Pro Gly Ala Thr Pro Asp Gly Val Glu Asp			
50	55	60	
Leu Trp Tyr Pro Ile Trp Asp Ala Lys Lys Arg Leu Asp Tyr Ser Val			
65	70	75	80
Arg Thr Pro Asp Glu Cys Val Ala Met Ile Ser Ala Asp Ser Thr Ala			
85	90	95	
Ala Leu Ala Met Leu Asp Leu Arg Phe Ile Ala Gly Asp Glu Asp Leu			
100	105	110	
Cys Ala Lys Thr Arg Arg Arg Ile Val Glu Lys Trp Arg Gln Glu Leu			
115	120	125	
Asn Lys Asn Phe Asp Ala Val Val Asp Thr Ala Ile Ala Arg Trp Arg			
130	135	140	
Arg Ser Gly Pro Val Val Ala Met Thr Arg Pro Asp Leu Lys His Gly			
145	150	155	160
Arg Gly Gly Leu Arg Asp Phe Glu Leu Ile Lys Ala Leu Ala Leu Gly			
165	170	175	
His Leu Cys Asn Val Pro Gln Leu Asp Thr Gln His Gln Leu Leu			
180	185	190	
Asp Ala Arg Thr Leu Leu His Val His Ala Arg Arg Ser Arg Asp Val			
195	200	205	
Leu Asp Pro Glu Phe Ala Val Asp Val Ala Met Asp Leu Gly Phe Val			
210	215	220	
Asp Arg Tyr His Leu Gly Arg Glu Ile Ala Asp Ala Ala Arg Ala Ile			
225	230	235	240
Asp Asp Gly Leu Thr Thr Ala Leu Ala Thr Ala Arg Gly Ile Leu Pro			
245	250	255	
Arg Arg Thr Gly Phe Ala Phe Arg Asn Ala Ser Arg Arg Pro Leu Asp			
260	265	270	
Leu Asp Val Val Asp Ala Asn Gly Thr Ile Glu Leu Ser Lys Lys Pro			
275	280	285	
Asp Leu Asn Asp Pro Ala Leu Pro Leu Arg Val Ala Ala Ala Ala			

US-162

290	295	300													
Thr	Thr	Gly	Leu	Pro	Val	Ala	Glu	Ser	Thr	Trp	Ala	Arg	Leu	Asn	Glu
305	310	315	320												
Cys	Pro	Pro	Leu	Pro	Glu	Pro	Trp	Pro	Ala	Asn	Ala	Ala	Gly	Asp	Phe
		325	330	335											
Phe	Arg	Ile	Leu	Ser	Ser	Pro	Lys	Asn	Ser	Arg	Arg	Val	Val	Lys	Asn
		340	345	350											
Met	Asp	Arg	His	Gly	Leu	Trp	Ser	Arg	Phe	Val	Pro	Glu	Trp	Asp	Arg
		355	360	365											
Ile	Lys	Gly	Leu	Met	Pro	Arg	Glu	Pro	Ser	His	Ile	Ser	Thr	Ile	Asp
	370	375	380												
Glu	His	Ser	Leu	Asn	Thr	Val	Ala	Gly	Cys	Ala	Leu	Glu	Thr	Val	Thr
	385	390	395	400											
Val	Ala	Arg	Pro	Asp	Leu	Leu	Val	Leu	Gly	Ala	Leu	Tyr	His	Asp	Ile
	405	410	415												
Gly	Lys	Gly	Phe	Pro	Arg	Pro	His	Glu	Gln	Val	Gly	Ala	Glu	Met	Val
	420	425	430												
Ala	Arg	Ala	Ala	Ser	Arg	Met	Gly	Leu	Asn	Leu	Arg	Asp	Arg	Ala	Ser
	435	440	445												
Val	Gln	Thr	Leu	Val	Ala	Glu	His	Thr	Ala	Val	Ala	Lys	Ile	Ala	Ala
	450	455	460												
Arg	Leu	Asp	Pro	Ser	Ser	Glu	Gly	Ala	Val	Asp	Lys	Leu	Leu	Asp	Ala
	465	470	475	480											
Val	Arg	Tyr	Asp	Leu	Val	Thr	Leu	Asn	Leu	Leu	Glu	Val	Leu	Thr	Glu
	485	490	495												
Ala	Asp	Ala	Lys	Ala	Thr	Gly	Pro	Gly	Val	Trp	Thr	Ala	Arg	Leu	Glu
	500	505	510												
His	Ala	Leu	Arg	Ile	Val	Cys	Lys	Arg	Ala	Arg	Asp	Arg	Leu	Thr	Asp
	515	520	525												
Ile	Arg	Pro	Val	Ala	Pro	Met	Ile	Ala	Pro	Arg	Ser	Glu	Ile	Gly	Leu
	530	535	540												
Val	Glu	Arg	Asp	Gly	Val	Phe	Thr	Val	Gln	Trp	His	Gly	Glu	Asp	Leu
	545	550	555	560											
His	Arg	Ile	Leu	Gly	Val	Ile	Tyr	Ala	Lys	Gly	Trp	Thr	Ile	Thr	Ala
	565	570	575												
Ala	Arg	Met	Leu	Ala	Asn	Gly	Gln	Trp	Ser	Ala	Glu	Phe	Asp	Val	Arg
	580	585	590												
Ala	Asn	Gly	Pro	Gln	Asp	Phe	Asp	Pro	Gln	His	Phe	Leu	Gln	Ala	Tyr
	595	600	605												
Gln	Ser	Gly	Val	Phe	Ser	Glu	Val	Pro	Ile	Pro	Ala	Pro	Gly	Ile	Thr
	610	615	620												
Ala	Thr	Phe	Trp	His	Gly	Asn	Thr	Leu	Glu	Val	Arg	Thr	Glu	Leu	Arg
	625	630	635	640											
Thr	Gly	Ala	Ile	Phe	Ala	Leu	Leu	Arg	Thr	Leu	Pro	Asp	Ala	Leu	Trp
	645	650	655												
Ile	Asn	Ala	val	Thr	Arg	Gly	Ala	Thr	Leu	Ile	Ile	Gln	Ala	Ala	Leu
	660	665	670												
Lys	Pro	Gly	Phe	Asp	Arg	Ala	Thr	Val	Glu	Arg	Ser	Val	Val	Arg	Ser
	675	680	685												
Leu	Ala	Gly	Ser												
	690														